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High rates of CTX-M-15-producing *Escherichia coli* and *Klebsiella pneumoniae* in wild boars and Barbary macaques in Algeria

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ABSTRACT

Objectives: The present study aimed to screen for the presence of extended-spectrum β-lactamase (ESBL)-producing Enterobacteriaceae in wild boars and Barbary macaques in Béjaïa and Jijel, Algeria.
Methods: A total of 216 faecal samples collected between September 2014 and August 2015 were cultured on MacConkey agar supplemented with 1 μg/mL ceftazidime. Isolates were identified by matrix-assisted laser desorption/ionisation time-of-flight mass spectrometry (MALDI-TOF/MS). Antimicrobial susceptibility testing was performed by the disk diffusion method, and ESBLs were characterised by PCR and sequencing. Clonal relatedness was studied by multilocus sequence typing (MLST).
Results: A total of 47 ESBL-producing isolates were recovered from faecal samples from 40 (44%) of 90 wild boars and 7 (6%) of 126 from Barbary macaques, including 30 *Escherichia coli* and 17 *Klebsiella pneumoniae*. Results of PCR and sequencing analysis showed that all of the isolates produced CTX-M-15, and 25 isolates co-produced TEM-1. MLST demonstrated the presence of eight sequence types (STs) among the *E. coli* isolates (ST617, ST131, ST648, ST405, ST1431, ST1421, ST69 and ST226), whereas only one clone (ST584) was identified for all isolates of *K. pneumoniae* recovered from wild boars ($n = 10$) and Barbary macaques ($n = 7$).
Conclusions: This is the first report of CTX-M-15-producing *E. coli* and *K. pneumoniae* in wild animals from Algeria. The results show that African wildlife can act as a reservoir of the epidemic *E. coli* clone ST131 producing CTX-M-15, suggesting that this lineage can survive in different ecological niches and adapt to different hosts.

1. Introduction

Resistance to antibiotics is continuously increasing. It is largely accepted that the massive use of antibiotics in human and veterinary medicine, aquaculture and agriculture contribute to the development and spread of antibiotic resistance [1]. The reservoir of resistance genes in the environment is due to a mix of naturally occurring resistance and those present in animal and human waste and the selective effects of pollutants, as well as antibiotic residues and other pollutants that can co-select for antibiotic resistance [2]. Increasingly, antimicrobial resistance has also been reported in wildlife that has not been exposed to contact with antibiotics [3,4].

Several studies have documented the occurrence of resistant or multiresistant bacteria in wild animals kept in zoos or sanctuaries [5,6], but less is known about animals living in nature reserves and protected regions [3]. The occurrence of cephalosporin-resistant Enterobacteriaceae producing extended-spectrum β-lactamases (ESBLs) in animals is particularly worrisome owing to the clinical importance of cephalosporins in human medicine [4,7]. Detection of ESBL-producing Enterobacteriaceae of wildlife origin dates back to 2006 [8]. Since then, numerous studies have reported the occurrence of ESBL-producing Enterobacteriaceae in wild animals such as wild fish [9], wild boars [10,11], wild rodents [12] and Iberian lynx [13].

The context of this study aims to provide more knowledge about the global dissemination of ESBL genes in wild animals that have consequences for the environment and public health. The aims of this study were to investigate the occurrence of

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ESBL-producing Enterobacteriaceae isolates from Barbary macaques and wild boars in Algeria (Béjaïa and Jijel) and to determine the clonal relatedness of the isolates by multilocus sequence typing (MLST).

2. Materials and methods

2.1. Study area and animals

Faecal samples were collected from September 2014 to August 2015 in Béjaïa (Gouraya National Park and Tichy) and Jijel (Taza National Park) in Algeria. Both parks are located on the Mediterranean coast. These two parks were established to protect the coastline and surrounding forests. Gouraya National Park is north-east of Béjaïa, close to the city. The park includes the mountain of Gouraya, which rises to 660 m. The park is situated 230 km from Algiers and 96 km east of Jijel, which is home to Taza National Park. The latter sits on the Mediterranean coast and includes cliffs that rise from sea level to over 1100 m. The largest forest in Algeria of cork oaks (*Quercus suber*) and gall oaks (*Quercus faginea*) is found in this park. Human activities such as fishing and hunting are controlled in these parks. Tourism is also important in these two national parks. These parks form a UNESCO-recognised biosphere reserve with a variety of flora and fauna, including Barbary macaques, which is the only macaque primate in north Africa, and wild boars, which are also native to north Africa (Fig. 1).

2.2. Sample collection and processing

In this study, Barbary macaques and wild boars were followed while walking through the forest. The sampling team waited for the animals to defecate and collected fresh faecal samples by swabbing, as described below.

A total of 216 faecal samples from 90 wild boars and 126 Barbary macaques (1 swab per animal) were collected by picking up a small amount of stool with a swab. All samples were transported under refrigeration temperature (4 °C) to the laboratory and were analysed within a maximum of 4 h. Swabs were cultured overnight at 37 °C in 10 mL of nutrient broth (Fluka, St. Louis, MO). For screening of ESBL-producing Enterobacteriaceae, 200 μL of the culture was streaked onto MacConkey agar plates (Fluka) supplemented with 1 μg/mL ceftazidime. Following overnight incubation at 37 °C, colonies displaying different morphology were cultured individually on trypticase soy agar (Fluka). Isolates were identified by matrix-assisted laser desorption/ionisation time-of-flight mass spectrometry (MALDI-TOF/MS) (Microflex; Bruker Daltonics, Bremen, Germany) [14].

The double-disk synergy test with cefotaxime, ceftazidime, cefepime and amoxicillin/clavulanic acid (AMC) disks was used for phenotypic confirmation of ESBL production [15].

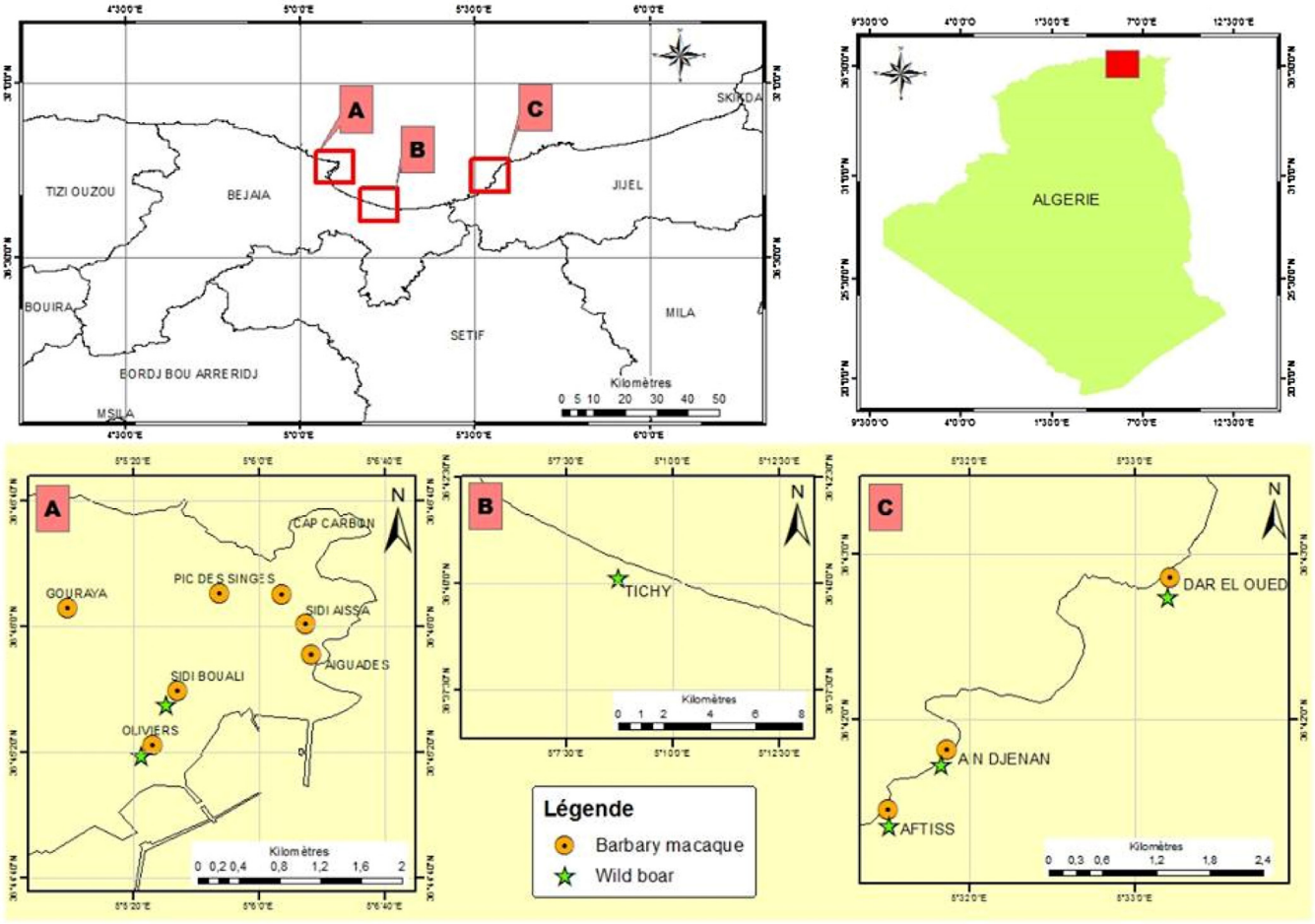

Fig. 1. Map showing the locations of faecal sampling from Barbary macaques and wild boars in different study sites (Gouraya National Park in Béjaïa and Taza National Park in Jijel) in Algeria: (A) Gouraya National Park (Béjaïa); (B) Tichy (Béjaïa); and (C) Jijel.

2.3. Antimicrobial susceptibility testing

Antibiotic susceptibility was determined on Mueller–Hinton agar (Fluka) using the standard disk diffusion procedure as described by the European Committee on Antimicrobial Susceptibility Testing (EUCAST) [16]. Eighteen antibiotics were tested, including amoxicillin (20 μg), amoxicillin/clavulanic acid (AMC) (20/10 μg), ticarcillin/clavulanic acid (TIM) (75/10 μg), imipenem (10 μg), ertapenem (10 μg), ceftriaxone (30 μg), trimethoprim/sulfamethoxazole (SXT) (25 μg), cefepime (30 μg), cefoxitin (30 μg), cefotaxime (30 μg), ceftazidime (30 μg), aztreonam (30 μg), fosfomycin (200 μg), amikacin (30 μg), gentamicin (15 μg), ciprofloxacin (5 μg), tetracycline (30 μg) and colistin (50 μg) (Bio-Rad, Hercules, CA). Isolates were classified as 'susceptible', 'intermediate' or 'resistant', according to EUCAST (2015) recommendations. *Escherichia coli* ATCC 25922 was used as a quality control strain.

2.4. Molecular characterisation of extended-spectrum β-lactamase genes

Molecular detection of the most prevalent ESBL genes encoding bla_{TEM},bla_{CTX-M} and bla_{SHV} was carried out by PCR amplification as previously described [17]. The PCR programme consisted of an initial denaturation at 94 °C for 3 min, followed by 30 cycles of denaturation at 94 °C for 30 s, annealing at 55 °C for SHV and TEM and at 51 °C for CTX-M for 30 s and extension at 72 °C for 1 min, and a final extension at 72 °C for 7 min [17].

2.5. Multilocus sequencing typing

MLST was performed using seven conserved housekeeping genes for *Klebsiella pneumoniae* (*pgiB*, *gap*, *tonB*, *mdh*, *phoE*, *infB* and *rpoB*) according to schemes available on the Institut Pasteur MLST website (http://www.pasteur.fr/mlst) and seven housekeeping genes for *E. coli* (*purA*, *icd*, *adk*, *fumC*, *recA*, *mdh* and *gyrB)* as described in the *E. coli* MLST database (http://mlst.warwick.ac.uk/mlst/dbs/Ecoli).

2.6. DNA sequencing

PCR products were purified and sequenced using BigDye® terminator chemistry on an ABI 3730 Automated Sequencer (Applied Biosystems, Foster City, CA). The sequences obtained were analysed using BlastN and BlastP against the National Center for Biotechnology Information (NCBI) database (http://www.ncbi.nlm.nih.gov).

3. Results

3.1. Barbary macaques

Amongst the 126 faecal samples collected from Barbary macaques within the two cities (Béjaïa and Jijel), 7 (6%) presumptive ESBL-producing *K. pneumoniae* were isolated and were confirmed by the double disk synergy test. No *E. coli* isolate producing ESBL was detected in this animal species.

The results of antibiotic susceptibility testing performed on these isolates demonstrated high resistance rates to almost antibiotics tested. All isolates (100%) were resistant to amoxicillin, AMC, TIM, ceftriaxone, cefotaxime, aztreonam, ceftazidime, SXT, gentamicin and ciprofloxacin, followed by cefepime (86%), fosfomycin (29%) and tetracycline (14%). All isolates were susceptible to cefoxitin, amikacin, imipenem, ertapenem and colistin.

DNA sequencing of the PCR products identified the $bla_{CTX-M-15}$ and bla_{TEM-1} genes in all seven isolates (Table 1). Interestingly, MLST analysis showed that all *K. pneumoniae* isolates recovered from the two parks were assigned to a unique sequence type (ST584) (Table 1).

3.2. Wild boars

Amongst the 90 faecal samples collected from wild boars, 40 (44%) presumptive ESBL-producing Enterobacteriaceae were isolated and were confirmed by the double-disk synergy test, including 10 *K. pneumoniae* and 30 *E. coli.*

All of these isolates (100%) were resistant to amoxicillin, TIM, ceftriaxone, ceftazidime, cefotaxime and aztreonam. Furthermore, several isolates were resistant to cefepime (90%), SXT (88%), ciprofloxacin (85%), AMC (75%), gentamicin (73%) tetracycline (70%), fosfomycin (3%) and amikacin (3%). Isolates were susceptible to cefoxitin, imipenem, ertapenem and colistin.

Molecular characterisation by PCR and DNA sequencing showed that all of the isolates harboured the $bla_{CTX-M-15}$ gene. In addition, the bla_{TEM-1} gene was observed in 18 isolates (8 *E. coli* isolates and all 10 *K. pneumoniae* isolates) (Table 2).

According to MLST analysis, the 30 *E. coli* isolates were assigned to eight STs, including ST617 ($n = 13$), ST648 ($n = 4$), ST405 ($n = 3$), ST131 ($n = 3$), ST1421 ($n = 2$), ST226 ($n = 2$), ST69 ($n = 2$) and ST1431 ($n = 1$). Interestingly, all *K. pneumoniae* isolates from wild boars belonged to the same ST (ST584) (Table 2), which was the same ST detected amongst isolates from Barbary macaques (Table 1).

4. Discussion

The emergence and spread of resistance among Enterobacteriaceae isolates is a serious threat to public health [18]. Reports of ESBL-producing Enterobacteriaceae have been increasing worldwide not only in human bacterial isolates but also in food-producing animals such as pigs, cattle and domestic fowl [10] as well as in pets [19], waste water [20] and wild animals [21]. This study constitutes the first report on the occurrence of multi-resistant *E. coli* and *K. pneumoniae* isolates from wild boars and Barbary macaques producing CTX-M-15-type ESBL in Africa. CTX-M-15 is the most prevalent ESBL type among clinical *E. coli* isolated from humans in many countries, but has been frequently reported in companion and wild animals as well as in samples of

Table 1
Characteristics of extended-spectrum β-lactamase (ESBL)-producing *Klebsiella pneumoniae* (Kp) isolates from Barbary macaques in Béjaïa and Jijel, Algeria.

Code	Isolate	Region	Phenotype pattern	ESBL gene	MLST
M034	Kp	Béjaïa	AMX-ATM-GEN-SXT-CAZ-AMC-CRO-CTX-TIM-CIP	CTX-M-15/TEM-1	ST584
M035	Kp	Jijel	AMX-ATM-GEN-SXT-CAZ-FEP-AMC-CRO-CTX-TIM-CIP	CTX-M-15/TEM-1	ST584
M032	Kp	Béjaïa	AMX-ATM-GEN-SXT-CAZ-FEP-AMC-CRO-CTX-TIM-CIP-TET	CTX-M-15/TEM-1	ST584
M037	Kp	Jijel	AMX-ATM-GEN-SXT-CAZ-FEP-AMC-CRO-CTX-TIM-CIP	CTX-M-15/TEM-1	ST584
M036	Kp	Jijel	AMX-ATM-GEN-SXT-CAZ-FEP-AMC-CRO-FOS-CTX-TIM-CIP	CTX-M-15/TEM-1	ST584
M038	Kp	Jijel	AMX-ATM-GEN-SXT-CAZ-FEP-AMC-CRO-FOS-CTX-TIM-CIP	CTX-M-15/TEM-1	ST584
M033	Kp	Jijel	AMX-ATM-GEN-SXT-CAZ-FEP-AMC-CRO-CTX-TIM-CIP	CTX-M-15/TEM-1	ST584

MLST, multilocus sequence typing; AMX, amoxicillin; ATM, aztreonam; GEN, gentamicin; SXT, trimethoprim/sulfamethoxazole; CAZ, ceftazidime; AMC, amoxicillin/clavulanic acid; CRO, ceftriaxone; CTX, cefotaxime; TIM, ticarcillin/clavulanic acid; CIP, ciprofloxacin; FEP, cefepime; TET, tetracycline; FOS, fosfomycin.

Table 2
Characteristics of extended-spectrum β-lactamase (ESBL)-producing *Escherichia coli* (Ec) and *Klebsiella pneumoniae* (Kp) isolates from wild boars in Béjaïa and Jijel, Algeria.

Code	Isolate	Region	Phenotype pattern	ESBL gene	MLST
B021	Ec	Béjaïa	AMX-ATM-SXT-CAZ-CRO-CTX-TIM-CIP-TET	CTX-M-15	ST617
B033	Ec	Béjaïa	AMX-ATM-SXT-CAZ-FEP-CRO-CTX-TIM-TET	CTX-M-15	ST617
B035	Ec	Béjaïa	AMX-ATM-GEN-SXT-CAZ-FEP-CRO-CTX-TIM-CIP-TET	CTX-M-15	ST617
B038	Ec	Béjaïa	AMX-ATM-GEN-SXT-CAZ-FEP-CRO-CTX-TIM-CIP-TET	CTX-M-15	ST617
B040	Ec	Béjaïa	AMX-ATM-GEN-SXT-CAZ-FEP-AMC-CRO-CTX-TIM-CIP-TET	CTX-M-15	ST617
B043	Ec	Béjaïa	AMX-ATM-GEN-SXT-CAZ-FEP-AMC-CRO-CTX-TIM-CIP-TET	CTX-M-15	ST617
B045	Ec	Béjaïa	AMX-ATM-GEN-SXT-CAZ-FEP-AMC-CRO-CTX-TIM-CIP-TET	CTX-M-15	ST617
B004	Ec	Béjaïa	AMX-ATM-GEN-SXT-CAZ-FEP-AMC-CRO-CTX-TIM-CIP-TET	CTX-M-15	ST617
B005	Ec	Béjaïa	AMX-ATM-GEN-SXT-CAZ-FEP-AMC-CRO-CTX-TIM-CIP-TET	CTX-M-15	ST617
B015	Ec	Béjaïa	AMX-ATM-GEN-SXT-CAZ-FEP-AMC-CRO-CTX-TIM-CIP-TET	CTX-M-15	ST617
B032	Ec	Béjaïa	AMX-ATM-GEN-SXT-CAZ-FEP-AMC-CRO-CTX-TIM-CIP-TET	CTX-M-15	ST617
B034	Ec	Béjaïa	AMX-ATM-GEN-SXT-CAZ-FEP-AMC-CRO-CTX-TIM-CIP-TET	CTX-M-15	ST648
B036	Ec	Béjaïa	AMX-ATM-GEN-SXT-CAZ-FEP-AMC-CRO-CTX-TIM-CIP-TET	CTX-M-15	ST648
B037	Ec	Béjaïa	AMX-ATM-GEN-SXT-CAZ-FEP-AMC-CRO-CTX-TIM-CIP-TET	CTX-M-15	ST648
B044	Ec	Béjaïa	AMX-ATM-GEN-SXT-CAZ-FEP-AMC-CRO-CTX-TIM-CIP-TET	CTX-M-15	ST648
B006	Ec	Béjaïa	AMX-ATM-GEN-CRO-CAZ-FEP-CTX-TIM-CIP-TET	CTX-M-15	ST131
B011	Ec	Béjaïa	AMX-ATM-GEN-AMC-CAZ-FEP-CRO-CTX-TIM-CIP	CTX-M-15	ST131
B008	Ec	Béjaïa	AMX-ATM-CRO-CTX-CAZ-FEP-TIM	CTX-M-15	ST226
B026	Ec	Béjaïa	AMX-ATM-AMC-CAZ-FEP-CRO-CTX-TIM-TET	CTX-M-15	ST226
B003	Ec	Béjaïa	AMX-ATM-GEN-SXT-CAZ-FEP-AMC-CRO-CTX-TIM-CIP-TET	CTX-M-15	ST405
B041	Ec	Béjaïa	AMX-ATM-GEN-SXT-CAZ-FEP-AMC-CRO-CTX-TIM-CIP-TET	CTX-M-15/TEM-1	ST617
B039	Ec	Béjaïa	AMX-ATM-SXT-CAZ-FEP-CRO-CTX-TIM-CIP-TET	CTX-M-15/TEM-1	ST1421
B042	Ec	Béjaïa	AMX-ATM-SXT-CAZ-FEP-CRO-CTX-TIM-CIP-TET	CTX-M-15/TEM-1	ST1421
B009	Ec	Béjaïa	AMX-ATM-SXT-CAZ-FEP-CRO-CTX-TIM-CIP-TET	CTX-M-15/TEM-1	ST1431
B017	Ec	Béjaïa	AMX-ATM-SXT-CAZ-FEP-CRO-CTX-TIM-TET	CTX-M-15/TEM-1	ST69
B029	Ec	Jijel	AMX-ATM-GEN-CAZ-SXT-AMC-CRO-CTX-TIM-CIP-TET	CTX-M-15	ST617
B010	Ec	Jijel	AMX-ATM-GEN-AMC-CAZ-FEP-CRO-CTX-TIM-CIP	CTX-M-15	ST131
B030	Ec	Jijel	AMX-ATM-SXT-CAZ-FEP-AMC-CRO-CTX-TIM-CIP-TET	CTX-M-15/TEM-1	ST405
B031	Ec	Jijel	AMX-ATM-SXT-CAZ-FEP-AMC-CRO-CTX-TIM-CIP-TET	CTX-M-15/TEM-1	ST405
B014	Ec	Jijel	AMX-ATM-SXT-CAZ-FEP-AMC-CRO-CTX-TIM-TET	CTX-M-15/TEM-1	ST69
B025	Kp	Jijel	AMX-ATM-GEN-SXT-CAZ-AMC-CRO-CTX-TIM-CIP	CTX-M-15/TEM-1	ST584
B016	Kp	Jijel	AMX-ATM-GEN-SXT-FEP-CAZ-AMC-CRO-CTX-TIM-CIP	CTX-M-15/TEM-1	ST584
B019	Kp	Jijel	AMX-ATM-GEN-SXT-AMC-FEP-CAZ-CRO-CTX-TIM	CTX-M-15/TEM-1	ST584
B022	Kp	Jijel	AMX-ATM-GEN-SXT-CAZ-AMC-CRO-CTX-TIM-CIP	CTX-M-15/TEM-1	ST584
B023	Kp	Jijel	AMX-ATM-GEN-SXT-FEP-CAZ-AMC-CRO-CTX-TIM-CIP-AMK	CTX-M-15/TEM-1	ST584
B028	Kp	Jijel	AMX-ATM-GEN-SXT-CAZ-FEP-AMC-CRO-CTX-TIM-CIP	CTX-M-15/TEM-1	ST584
B027	Kp	Jijel	AMX-ATM-GEN-SXT-CAZ-FEP-AMC-CRO-CTX-TIM-CIP	CTX-M-15/TEM-1	ST584
B024	Kp	Jijel	AMX-ATM-GEN-SXT-CAZ-FEP-AMC-CRO-FOS-CTX-TIM-CIP	CTX-M-15/TEM-1	ST584
B018	Kp	Béjaïa	AMX-ATM-GEN-SXT-CAZ-FEP-AMC-CRO-CTX-TIM-CIP	CTX-M-15/TEM-1	ST584
B007	Kp	Béjaïa	AMX-ATM-GEN-SXT-CAZ-FEP-AMC-CRO-CTX-TIM-CIP-TET	CTX-M-15/TEM-1	ST584

MLST, multilocus sequence typing; AMX, amoxicillin; ATM, aztreonam; SXT, trimethoprim/sulfamethoxazole; CAZ, ceftazidime; CRO, ceftriaxone; CTX, cefotaxime; TIM, ticarcillin/clavulanic acid; CIP, ciprofloxacin; TET, tetracycline; FEP, cefepime; GEN, gentamicin; AMC, amoxicillin/clavulanic acid; AMK, amikacin; FOS, fosfomycin.

environmental origin [22,23]. Other ESBL types, mainly CTX-M-1 and CTX-M-14, are currently regarded as the most prevalent ESBL types in livestock species [24,25].

A prevalence of ESBL faecal carriage of 44% was found in wild boars. This rate is higher than that reported by Poeta et al. (10.4%) and Literak et al. (2%) who described *E. coli* isolates producing CTX-M-1 group from wild boars in Portugal and the Czech Republic, respectively [10,11]. Furthermore, to our knowledge, no previous studies have reported the presence of ESBLs in *K. pneumoniae* in Barbary macaques until now. In the current study, the prevalence of ESBL faecal carriage in Barbary macaques was 6%. A higher prevalence rate (32%) has been reported among *E. coli* isolates from other species of monkey in China, including strains harbouring $bla_{\text{CTX-M-3}}$, $bla_{\text{CTX-M-14}}$ and $bla_{\text{CTX-M-15}}$ [26]. Janatova et al. also described CTX-M-15-producing *K. pneumoniae* isolated from a gorilla in the Central African Republic [27].

In this study, CTX-M-15-producing *E. coli* isolated from wild boars mainly belonged to ST617, a ST that contributes to the spread of various ESBL and *ampC* genes and that is widely described in relation to hospital-acquired infections as well as in commensal *E. coli* strains isolated in humans, animals and food-producing animals [4]. We also report CTX-M-15-producing *E. coli* isolates from wild boars with several STs, including the presence of ST131 and ST405, which are multidrug-resistant virulent clones involved in the intercontinental dissemination of $bla_{\text{CTX-M-15}}$ [4]. The hypervirulent *E. coli* ST131 harbours a wide range of virulence genes and various plasmid-mediated resistance genes and is involved in the global spread of CTX-M-15 [28]. The ST131 clone is identified in pets, poultry, livestock, food and wild animals and is known to be associated with community-onset infections in humans, including urinary tract infections, bacteraemia and neonatal sepsis [4,29].

E. coli ST405 has been described in association with various CTX-M types worldwide and was also reported to be associated with New Delhi metallo-β-lactamases (NDMs) in *E. coli* isolates in rooks, wild ducks [4], domestic birds [27] and humans [30]. Consequently, this finding confirms that some *E. coli* clones can persist and spread between wild species and might have a remarkable impact to native flora and fauna. The other STs described for *E. coli* isolates from wild boar in this study were ST648, ST69, ST1431, ST1421 and ST226. These clones have also been detected in human patients, the environment and wildlife [20,21,31–33]. Therefore, we suggest that wild boars can act as a reservoir for a long list of zoonotic bacterial agents.

In this study, the ST584 clone was identified in all isolates of *K. pneumoniae* recovered from wild boars and Barbary macaques. Dolejska et al. reported *K. pneumoniae* ST584 carrying $bla_{\text{IMP-4}}$ in silver gulls in Australia [34]. Furthermore, it has previously been demonstrated that migrating birds and seagulls appear to act as transporters or reservoirs of resistant bacteria and may consequently play an important role in the circulation of epidemiologically significant clones and may pose a risk for environmental

contamination [35]. Intestinal bacteria may also be easily disseminated throughout various ecosystems through water [21]. Accordingly, identification of the ST584 clone in the isolates in this study may be due to an exchange of bacteria with wild birds whose faeces can contaminate food and water sources shared both by wild boars and Barbary macaques. Other possible means for the transmission of CTX-M-15-carrying strains and plasmids may include the proximity of wild animals to human settlements [36,37], wild rodents [2,38] and manure spreading in agriculture [7].

This study has some limitations, including the sensitivity of the screening method used. Ceftazidime is not the best cephalosporin for detecting ESBLs of the CTX-M-type, which might explain the lack of detection of CTX-M types other than CTX-M-15 [39].

To the best of our knowledge, this is the first report of CTX-M-15-producing *E. coli* and *K. pneumoniae* in wild animals from Algeria, including a common clone of CTX-M-15-producing *K. pneumoniae* shared by macaques and wild boars from the same national parks. The results show that African wildlife can act as a reservoir of the epidemic *E. coli* clone ST131 producing CTX-M-15, suggesting that this lineage can survive in different ecological niches and adapt to different hosts. In-depth molecular characterisation of the CTX-M-15 clonal types shared by different animal species and humans in the region is warranted to assess clone evolution and possible interspecies transmission.

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Competing interest

None declared.

Ethical approval

Not required.

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